

### **Biostatistics statement**

All experimental data were analyzed using SPSS software (version 22.0; IBM, Armonk, NY, United States) and GraphPad Prism 5.0 (GraphPad Software, La Jolla, CA, United States). The expression level of each circRNA was represented as fold-change using the  $2^{-\Delta\Delta Ct}$  method on qRT-PCR analysis. Differences of hsa\_circ\_0000745 levels between GC tissues and adjacent non-tumor tissues, and between plasma from patients with GC and plasma from healthy controls were assessed using *t*-test. The correlation between hsa\_circ\_0000745 levels and clinicopathological factors was further analyzed by one-way analysis of variance. The receiver operating characteristic (ROC) curve was established to evaluate the diagnostic value. The cut-off value of hsa\_circ\_0000745 was analyzed by the SPSS software. A *P* value < 0.05 was considered to be statistically significant.